SEQUENCE LISTING

<110> OHTAKI, Hiromi
NAKAMURA, Jun
IZUI, Hiroshi
NAKAMATSU, Tsuyoshi

<120> Bacterium Producing L-Glutamic Acid and Method for Producing L-Glutamic Acid

<130> OP1195

<140>
<141> 2000-07-

<150> JP 2000-204256
<151> 2000-07-05

<160> 34

<170> PatentIn Ver. 2.0

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caagtggaat tctgcagcgg 20

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tgagttttta gaagactccc 20

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cgcttcagtg gtgttgtccc 20

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<400> 28
cgtaccactc cacggaaatt cccg 24

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<213> Brevibacterium lactofermentum

<220>
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<222> (484)..(1938)

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aaaatcaacc tgcttaggcg tctttcgctt aaatagcgta gaatatcggg tcgatcgctt 120
ttaaacactc aggaggatcc ttgccggcca aaatcacgga cactcgtccc accccagaat 180
cccttcacgc tgttgaagag gaaaccgcag ccggtgcccg caggattgtt gccacctatt 240
ctaaggactt cttcgacggc gtcactttga tgtgcatgct cggcgttgaa cctcagggcc 300
tgcgttacac caaggtcgct tctgaacacg aggaagctca gccaaagaag gctacaaagc 360
ggactcgtaa ggctaccagc taagaaggct gctgctaaga aaacgaccaa gaagaccact 420
aagaaaacta ctaaaaagac caccgcaaag aagaccacaa agaagtctta agccggatct 480
tat atg gat gat tcc aat agc ttt gta gtt gtt gct aac cgt ctg cca 528
Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro

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1               5                  10                 15
gtg gat atg act gtc cac cca gat ggt agc tat agc atc tcc ccc agc    576
Val Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser
                20                 25                 30
ccc ggt ggc ctt gtc acg ggg ctt tcc ccc gtt ctg gaa caa cat cgt    624
Pro Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg
            35                 40                 45
gga tgt tgg gtc gga tgg cct gga act gta gat gtt gca ccc gaa cca    672
Gly Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro
        50                 55                 60
ttt cga aca gat acg ggt gtt ttg ctg cac cct gtt gtc ctc act gca    720
Phe Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala
    65                 70                 75
agt gac tat gaa ggc ttc tac gag ggc ttt tca aac gca acg ctg tgg    768
Ser Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp
80                 85                 90                  95
cct ctt ttc cac gat ctg att gtt act ccg gtg tac aac acc gat tgg    816
Pro Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp
                100                105                110
tgg cat gcg ttt cgg gaa gta aac ctc aag ttc gct gaa gcc gtg agc    864
Trp His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser
            115                120                125
caa gtg gcg gca cac ggt gcc act gtg tgg gtg cag gac tat cag ctg    912
Gln Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu
        130                135                140
ttg ctg gtt cct ggc att ttg cgc cag atg cgc ctt gat ttg aag atc    960
Leu Leu Val Pro Gly Ile Leu Arg Gln Met Arg Leu Asp Leu Lys Ile
    145                150                155
ggt ttc ttc ctc cac att ccc ttc cct tcc cct gat ctg ttc cgt cag    1008
Gly Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln
160                165                170                175
ctg ccg tgg cgt gaa gag att gtt cga ggc atg ctg ggc gca gat ttg    1056
Leu Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu
                180                185                190
gtg gga ttc cat ttg gtt caa aac gca gaa aac ttc ctt gcg tta acc    1104
Val Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr
            195                200                205
cag cag gtt gcc ggc act gcc ggg tct cat gtg ggt cag ccg gac acc    1152
Gln Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr
        210                215                220
ttg cag gtc agt ggt gaa gca ttg gtg cgt gag att ggc gct cat gtt    1200
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Leu Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val
    225                 230                 235
gaa acc gct gac gga agg cga gtt agc gtc ggg gcg ttc ccg atc tcg   1248
Glu Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser
240                 245                 250                 255
att gat gtt gaa atg ttt ggg gag gcg tcg aaa agc gcc gtt ctt gat   1296
Ile Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp
                260                 265                 270
ctt tta aaa acg ctc gac gag ccg gaa acc gta ttc ctg ggc gtt gac   1344
Leu Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp
            275                 280                 285
cga ctg gac tac acc aag ggc att ttg cag cgc ctg ctt gcg ttt gag   1392
Arg Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu
        290                 295                 300
gaa ctg ctg gaa tcc ggc gcg ttg gag gcc gac aaa gct gtg ttg ctg   1440
Glu Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu
    305                 310                 315
cag gtc gcg acg cct tcg cgt gag cgc att gat cac tat cgt gtg tcg   1488
Gln Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser
320                 325                 330                 335
cgt tcg cag gtc gag gaa gcc gtc ggc cgt atc aat ggt cgt ttc ggt   1536
Arg Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly
                340                 345                 350
cgc atg ggg cgt ccc gtg gtg cat tat cta cac agg tca ttg agc aaa   1584
Arg Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys
            355                 360                 365
aat gat ctc cag gtg ctg tat acc gca gcc gat gtc atg ctg gtt acg   1632
Asn Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr
        370                 375                 380
cct ttt aaa gac ggt atg aac ttg gtg gct aaa gaa ttc gtg gcc aac   1680
Pro Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn
    385                 390                 395
cac cgc gac ggc act ggt gct ttg gtg ctg tcc gaa ttt gcc ggc gcg   1728
His Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala
400                 405                 410                 415
gcc act gag ctg acc ggt gcg tat tta tgc aac cca ttt gat gtg gaa   1776
Ala Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu
                420                 425                 430
tcc atc aaa cgg caa atg gtg gca gct gtc cat gat ttg aag cac aat   1824
Ser Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn
            435                 440                 445
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ccg gaa tct gcg gca acg cga atg aaa acg aac agc gag cag gtc tat   1872
Pro Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr
        450                 455                 460
acc cac gac gtc aac gtg tgg gct aat agt ttc ctg gat tgt ttg gcg   1920
Thr His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala
    465                 470                 475
cag tcg gga gaa aac tca tgaaccgcgc acgaatcgcg accataggcg          1968
Gln Ser Gly Glu Asn Ser
480                 485
ttcttccgct tgctttactg ctggcgtcct gtggttcaga caccgtggaa atgacagatt 2028
ccacctggtt ggtgaccaat atttacaccg atccagatga gtcgaattcg atcagtaatc 2088
ttgtcatttc ccagcccagc ttagattttg gcaattcttc cctgtctggt ttcactggct 2148
gtgtgccttt tacggggcgt gcggaattct tccaaaatgg tgagcaaagc tctgttctgg 2208
atgccgatta tgtgaccttg tcttccctgg atttcgataa acttcccgat gattgccaag 2268
gacaagaact caaagttcat aacgagctgg ttgatcttct gcctggttct tttgaaatct 2328
ccaggacttc tggttcagaa atcttgctga ctagcgatgt c                    2369

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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
             20                  25                  30
Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
         35                  40                  45
Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
     50                  55                  60
Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
 65                  70                  75                  80
Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
                 85                  90                  95
Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
            100                 105                 110
His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
        115                 120                 125
Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
    130                 135                 140
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Leu Val Pro Gly Ile Leu Arg Gln Met Arg Leu Asp Leu Lys Ile Gly
145   150   155   160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
                165   170   175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
            180   185   190

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
        195   200   205

Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
    210   215   220

Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
225   230   235   240

Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
                245   250   255

Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
            260   265   270

Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
        275   280   285

Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
    290   295   300

Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln
305   310   315   320

Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
                325   330   335

Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
            340   345   350

Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
        355   360   365

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
    370   375   380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
385   390   395   400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
                405   410   415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
            420   425   430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
        435   440   445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
    450   455   460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln

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465                 470                 475                 480
Ser Gly Glu Asn Ser
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<213> Brevibacterium lactofermentum

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<222> (82)..(2514)

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<222> (2953)
<223> n=a or g or c or t

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aacttttaag ggtgtttcat c atg gca cgt cca att tcc gca acg tac agg   111
                       Met Ala Arg Pro Ile Ser Ala Thr Tyr Arg
                         1               5                  10
ctt caa atg cga gga cct caa gca gat agc gcc ggg cgt ttc ttt ggt   159
Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala Gly Arg Phe Phe Gly
                15                  20                  25
ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg aag aag cta ggc atc   207
Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile
            30                  35                  40
agc cac ctg tac ctc tcc cct att ttt acg gcc atg cca gat tcc aat   255
Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala Met Pro Asp Ser Asn
        45                  50                  55
cat ggc tac gat gtc att gat ccc acc gcc atc aat gaa gag ctc ggt   303
His Gly Tyr Asp Val Ile Asp Pro Thr Ala Ile Asn Glu Glu Leu Gly
    60                  65                  70
ggc atg gag ggt ctt cga gat ctt gct gca gct aca cac gag ttg ggc   351
Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala Thr His Glu Leu Gly
 75                  80                  85                  90
atg ggc atc atc att gat att gtt ccc aac cat tta ggt gtt gcc gtt   399
Met Gly Ile Ile Ile Asp Ile Val Pro Asn His Leu Gly Val Ala Val
                95                  100                 105
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cca cat ttg aat cct tgg tgg tgg gat gtt cta aaa aac ggc aaa gat   447
Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu Lys Asn Gly Lys Asp
            110                 115                 120
tcc gct ttt gag ttc tat ttc gat att gac tgg cac gaa gac aac ggt   495
Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp His Glu Asp Asn Gly
        125                 130                 135
tct ggt ggc aag ctg ggc atg ccg att ctg ggt gct gaa ggc gat gaa   543
Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly Ala Glu Gly Asp Glu
    140                 145                 150
gac aag ctg gaa ttc gcg gag ctt gat gga gag aaa gtg ctc aaa tat   591
Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr
155                 160                 165                 170
ttt gac cac ctc ttc cca atc gcg cct ggt acc gaa gaa ggg aca ccg   639
Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro
                175                 180                 185
caa gaa gtc tac aag cgc cag cat tac cgc ctg cag ttc tgg cgc gac   687
Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu Gln Phe Trp Arg Asp
            190                 195                 200
ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg aat acg ttg gct ggc   735
Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val Asn Thr Leu Ala Gly
        205                 210                 215
atc agg caa gaa gat ccc ttg gtg ttt gaa cat act cat cgt ctg ctg   783
Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His Thr His Arg Leu Leu
    220                 225                 230
cgc gaa ttg gtg gcg gaa gac ctc att gac ggc gtg cgc gtc gat cac   831
Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly Val Arg Val Asp His
235                 240                 245                 250
ccc gac ggg ctt tcc gat cct ttt gga tat ctg cac aga ctc cgc gac   879
Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu His Arg Leu Arg Asp
                255                 260                 265
ctc att gga cct gac cgc tgg ctg atc atc gaa aag atc ttg agc gtt   927
Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu Lys Ile Leu Ser Val
            270                 275                 280
gat gaa cca ctc gat ccc cgc ctg gcc gtt gat ggc acc act ggc tac   975
Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr
        285                 290                 295
gac ccc ctc cgt gaa ctc gac ggc gtg ttt atc tcc cga gaa tct gag   1023
Asp Pro Leu Arg Glu Leu Asp Gly Val Phe Ile Ser Arg Glu Ser Glu
    300                 305                 310
gac aaa ttc tcc atg ttg gcg ctg acc cac agt gga tcc acc tgg gat   1071
Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser Gly Ser Thr Trp Asp
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315                 320                 325                 330
gaa cgc gcc cta aaa tcc acg gag gaa agc ctc aaa cga gtc gtc gcg   1119
Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu Lys Arg Val Val Ala
                335                 340                 345
caa caa gaa ctc gca gcc gaa atc tta agg ctc gcc cgc gcc atg cgc   1167
Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu Ala Arg Ala Met Arg
            350                 355                 360
cgc gat aac ttc tcc acc gca ggc acc aac gtc acc gaa gac aaa ctt   1215
Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val Thr Glu Asp Lys Leu
        365                 370                 375
agc gaa acc atc atc gaa tta gtc gcc gcc atg ccc gtc tac cgc gcc   1263
Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met Pro Val Tyr Arg Ala
    380                 385                 390
gac tac atc tcc ctc tca cgc acc acc gcc acc gtc atc gcg gag atg   1311
Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr Val Ile Ala Glu Met
395                 400                 405                 410
tcc aaa cgc ttc ccc tcc cgg cgc gac gca ctc gac ctc atc tcg gcc   1359
Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu Asp Leu Ile Ser Ala
                415                 420                 425
gcc cta ctt ggc aat ggc gag gcc aaa atc cgc ttc gcc caa gtc tgc   1407
Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg Phe Ala Gln Val Cys
            430                 435                 440
ggc gcc gtc atg gcc aaa ggt gtg gaa gac acc acc ttc tac cgc gca   1455
Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala
        445                 450                 455
tct agg ctc gtt gca ctg caa gaa gtc ggt ggc gcg ccg ggc agg ttc   1503
Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly Ala Pro Gly Arg Phe
    460                 465                 470
ggc gtc tcc gct gca gaa ttc cac ttg ctg cag gaa gaa cgc agc ctg   1551
Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln Glu Glu Arg Ser Leu
475                 480                 485                 490
ctg tgg cca cgc acc atg acc acc ttg tcc acg cac gac acc aaa cgc   1599
Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr His Asp Thr Lys Arg
                495                 500                 505
ggc gaa gat acc cgc gcc cgc atc atc tcc ctg tcc gaa gtc ccc gat   1647
Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu Ser Glu Val Pro Asp
            510                 515                 520
atg tac tcc gag ctg gtc aat cgt gtt ttc gca gtg ctc ccc gcg cca   1695
Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala Val Leu Pro Ala Pro
        525                 530                 535
gac ggc gca acg ggc agt ttc ctc cta caa aac ctg ctg ggc gta tgg   1743
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Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn Leu Leu Gly Val Trp
    540                 545                 550
ccc gcc gac ggc gtg atc acc gat gcg ctg cgc gat cga ttc agg gaa   1791
Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu
555                 560                 565                 570
tac gcc cta aaa gct atc cgc gaa gca tcc aca aaa acc acg tgg gtg   1839
Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr Lys Thr Thr Trp Val
                575                 580                 585
gac ccc aac gag tcc ttc gag gct gcg gtc tgc gat tgg gtg gaa gcg   1887
Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys Asp Trp Val Glu Ala
            590                 595                 600
ctt ttc gac gga ccc tcc acc tca tta atc acc gaa ttt gtc tcc cac   1935
Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr Glu Phe Val Ser His
        605                 610                 615
atc aac cgt ggc tct gtg aat atc tcc tta ggt agg aaa ctg ctg caa   1983
Ile Asn Arg Gly Ser Val Asn Ile Ser Leu Gly Arg Lys Leu Leu Gln
    620                 625                 630
atg gtg ggc gct gga atc ccc gac act tac caa gga act gag ttt tta   2031
Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu
635                 640                 645                 650
gaa gac tcc ctg gta gat ccc gat aac cga cgc ttt gtt gat tac acc   2079
Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr
                655                 660                 665
gcc aga gaa caa gtc ctg gag cgc ctg caa acc tgg gat tgg acg cag   2127
Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln
            670                 675                 680
gtt aat tcg gta gaa gac ttg gtg gat aac gcc gac atc gcc aaa atg   2175
Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala Asp Ile Ala Lys Met
        685                 690                 695
gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct gaa ttt cgt gca agc   2223
Ala Val Val His Lys Ser Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser
    700                 705                 710
ttt gtt ggt gga gat cat cag gca gta ttt ggc gaa ggt cgc gca gaa   2271
Phe Val Gly Gly Asp His Gln Ala Val Phe Gly Glu Gly Arg Ala Glu
715                 720                 725                 730
tcc cac atc atg ggc atc gcc cgc ggt aca gac cga aac cac ctc aac   2319
Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp Arg Asn His Leu Asn
                735                 740                 745
atc att gct ctt gct acc cgt cga cca ctg atc ttg gaa gac cgt ggc   2367
Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly
            750                 755                 760
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gga tgg tat gac acc acc gtc acg ctt cct ggt gga caa tgg gaa gac   2415
Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly Gly Gln Trp Glu Asp
        765                 770                 775
agg ctc acc ggg caa cgc ttc agt ggt gtt gtc cca gcc acc gat ttg   2463
Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val Pro Ala Thr Asp Leu
    780                 785                 790
ttc tca cat tta ccc gta tct ttg ttg gtt tta gta ccc gat agt gag   2511
Phe Ser His Leu Pro Val Ser Leu Leu Val Leu Val Pro Asp Ser Glu
795                 800                 805                 810
ttt tgatccctgc acaggaaagt tagcggcgct actatgaacg atcgatatgt        2564
Phe
ctgacaacac tctctcccaa tttggcagtt actaccacga attccgacgt gcccatccca 2624
tggccgacgt cgaattcctc ctagcaattg aagaattact cacagacggt ggtgtcacct 2684
tcgatcgcgt caccacacgc atcaaagaat ggtcaagcct gaaagccaag gctcgcaagc 2744
gtcgcgacga tggctcgttg atctaccctg atccgcgcaa agacatccac gacatgatcg 2804
gtgttcggat caccacgtac cactccacgg aaattcccgt ggccttaaaa gtgctccaag 2864
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<213> Brevibacterium lactofermentum

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Met Ala Arg Pro Ile Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro
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Gln Ala Asp Ser Ala Gly Arg Phe Phe Gly Phe Ala Gln Ala Lys Ala
             20                  25                  30
Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser
         35                  40                  45
Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
     50                  55                  60
Asp Pro Thr Ala Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
 65                  70                  75                  80
Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
                 85                  90                  95
Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
            100                 105                 110
Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
        115                 120                 125
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Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
    130   135   140
Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
145   150   155   160
Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
                165   170   175
Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
            180   185   190
Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
        195   200   205
Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro
    210   215   220
Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu
225   230   235   240
Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
                245   250   255
Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
            260   265   270
Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
        275   280   285
Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Pro Leu Arg Glu Leu
    290   295   300
Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu
305   310   315   320
Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser
                325   330   335
Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala
            340   345   350
Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr
        355   360   365
Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
    370   375   380
Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser
385   390   395   400
Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
                405   410   415
Arg Arg Asp Ala Leu Asp Leu Ile Ser Ala Ala Leu Leu Gly Asn Gly
            420   425   430
Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys
        435   440   445
Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu

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    450                 455                 460
Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
465                 470                 475                 480
Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
                485                 490                 495
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
            500                 505                 510
Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
        515                 520                 525
Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser
    530                 535                 540
Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
545                 550                 555                 560
Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
                565                 570                 575
Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
            580                 585                 590
Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
        595                 600                 605
Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
    610                 615                 620
Asn Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
625                 630                 635                 640
Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
                645                 650                 655
Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
            660                 665                 670
Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp
        675                 680                 685
Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
    690                 695                 700
Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His
705                 710                 715                 720
Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
                725                 730                 735
Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
            740                 745                 750
Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
        755                 760                 765
Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
    770                 775                 780
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Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe
805 810

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<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 33
ccaaaatcga taacatcaat cgagatcggg 30

<210> 34
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 34
cttgatcgat taaaaacgct cgacgagccg 30